

OM of: US-09-805-550-2 to: N.Geneseq_032802:* out_format : pfs
Date: Aug 31, 2002 7:40 AM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

-MODEL=frame+p2n.model -DEV=x1h
-O=/cgn2_1/USPRO.spool/US09805550/runtc_29082002_160820_307/app-query.fasta_1.897
-DB=N.Geneseq_032802 -OFMT=fastq -SUFFIX=oligop2n.rng
-GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPEXT=0.000
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-XGAPEXT=60.000 -FEAPOP=6.000 -FEAPEXT=7.000 -YGAPOP=60.000
-YGAEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=oligo -TRANS=human40.cdl -LIST=45 -DOCALLGN=200
-THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09805550 -CGN1_1.0 -NCPY=6 -ICPY=3 -LONGLOG
-DEV=TIMEOUT=120 -WARN=TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-805-550-2
Query length: 405
Database: N.Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 297.440000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

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AC AAD01230;
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XX 04-OCT-2000 (first entry)
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DE Maize Rad23 protein #1 encoding CDNA.
XX
KW Rad23; maize; ATCC No: PRA-530; recombinant expression cassette; wheat;
transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
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XX 12-OCT-1999; 99MO-US24129.
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XX 23-NOV-1998; 98US-0109728.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Mahajan PB, Tagliani L;
XX
XX WPI, 2000-40078/34.
XX
XX P-PSDB; AAY71458.
XX
XX Isolated nucleic acid encoding maize Rad23 protein is used to modulate
the levels of polypeptides in plant or in assays for identifying
compounds that bind to and/or increase/decrease enzymatic activity of
catalytically active polypeptides -
XX
XX Claim 1e; Page 73-75; 82pp; English.
XX
XX The present sequence is the cDNA encoding maize Rad23 protein #1. It is
isolated from V5 root tissue of a Zea mays cell line B73, infected with
corn root worm. This cDNA is deposited under the ATCC No: PRA-530. Maize
Rad23 DNA sequence operably linked to a promoter can be used to construct
a recombinant expression cassette. This expression cassette can be used
to generate a dicot or monocot transgenic plant e.g., maize, soybean,
sunflower, sorghum, canola, wheat, etc.. It can also be used to modulate
the levels of Rad23 polypeptide expression in a plant or in assays to
identify compounds, that bind to and/or modulate the enzymatic activity
of catalytically active polypeptides.
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Ratio: 1.000 Gaps: 0
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Align seg 1/1 to: AAD01230 from: 1 to: 1522

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108 GAGCCCCGATGCATCGCTTGATGTGAAGAGATCATGTGAGACCAACATC 157
34 InglyInSerThrTyrrArgAlaAspGlnGlnMetLeuIleTyrrGlnGly 50
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308 GTTCTACCGCTACTACTGCAAAAGCTCTGCAACTCTGGCCCAACTGCT 357
101 AlaProValAlaProAlaAlaSerValAlaArgThrProThrGlnAlaPr 117
358 GCCCGCTGGCCCTGCTGCTGATGAGTTCAGAGAACCAACACAGGCTCC 407
117 oValAlaThrAlaGluThrAlaProProSerValGlnProGlnAlaAlaP 134
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151 AlaSerAsnLeuValPheGlyAsnAsnLeuGluGlnThrIleGlnGlnI 167
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267 lValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProG 284
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317 eGlnGluAsnGlnAlaGluPheLeuArgLeuValaAsnGluSerProGlu 334
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
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PM EP1033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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926 AACCCCAATTCCTCAGCCCATGCTTCAGAACTTGAAAGCAAAACCC 975

311 ogln 312
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976 TCNA 979

seq_name: /SIDS1/gcgdata/geneseq/geneseqn_emb1/NA2000.DAT.AAA31521
seq_documentation_block:
ID AAA31521 standard; DNA; 480 BP.
XX
AC AAA31521;
XX
DT 05-JUL-2000 (first entry)
XX
DE Plant microsatellite marker #482.
XX
KW Plant microsatellite sequence; core repeat sequence; detection; probe;
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
PN WO9967421-A1.
XX
PD 29-DEC-1999.
XX
PF 25-JUN-1999; 99WO-NZ00092.
XX
PR 25-JUN-1998; 98US-0105307.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Havukkala IJ, Blokeberg LN, Glenn M;
XX
DR WPI: 2000-116958/10.

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XX New plant microsatellite markers and associated flanking species for
PT the detection of polymorphic genetic markers -
XX
XX
PS Claim 1, Page 219; 392pp; English.
XX
CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC and associated flanking species. The sequences comprise a central core
CC repeat sequence, especially selected from the sequences AAA32094-A32096
CC with left and right flanking sequences. The polynucleotide sequences
CC can be used in the detection of DNA polymorphisms, in genome mapping,
CC in physical mapping, in positional cloning of genes, in variety
CC identification and in evaluation of genetic variability within and
CC between plant tissues, populations, cultivars, species and species
CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are
CC useful to locate specific economically useful genes in plant genomes.
XX
SQ Sequence 480 BP; 136 A; 110 C; 130 G; 104 T; 0 other;

alignment_scores:
Quality: 13.00 Length: 13
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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176 AACGTCAAGACTCTGAGGCGACCACTTCGAATCCAA 214

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seq_documentation_block:
ID AAC44960 standard; DNA; 850 BP.
XX
AC AAC44960;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44778.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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751 GGTCCAAACGCAATTCATTAAACCTTCCTCCCAAGGC 789

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XX
AC AAD01231;
XX
DT 04-OCT-2000 (first entry)
XX
DE Maize Rad23 protein #2 encoding cDNA.
XX
KW Rad23; maize; ATCC No: PTA-531; recombinant expression cassette; wheat;
transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
XX
OS Zea mays.
XX
XX
Key Location/Qualifiers
FH 106..1222
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FT /*note= "Contained in ATCC No: PTA-531"
FT
XX
XX WO200031268-A1.
XX
XX PD 02-JUN-2000.
XX
XX PF 12-OCT-1999; 99WO-US24129.
XX
XX PR 23-NOV-1998; 98US-0109728.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Mahajan PB, Taglianti L;
XX
XX WPI; 2000-400078/34.
XX
XX DR P-PSDB; AAY71459.
XX
XX PT Isolated nucleic acid encoding maize RAD23 protein is used to modulate

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PT the levels of polypeptides in plant or in assays for identifying
PT compounds that bind to and/or increase/decrease enzymatic activity of
PT catalytically active polypeptides -
XX
PS Claim 1e; Page 76-78; 82pp; English.
XX
CC The present sequence is the cDNA encoding maize Rad3 protein #2. It is
CC isolated from a Zea mays cell line, B73 callus tissue regenerated five
CC days after transfer of the callus from medium containing auxin to a
CC medium devoid of exogenous auxin. This cDNA is deposited under the ATCC
CC No. PTA-531. Maize Rad3 DNA sequence operably linked to a promoter, can
CC be used to construct a recombinant expression cassette. This expression
CC cassette can be used to generate a dicot or monocot transgenic plant
CC e.g., maize, soybean, sunflower, sorghum, canola, wheat, etc.. It can
CC also be used to modulate the levels of Rad3 polypeptide expression in a
CC plant or in assays to identify compounds, that bind to and/or modulate
CC the enzymatic activity of catalytically active polypeptides.
XX
SQ Sequence 1702 BP; 490 A; 373 C; 432 G; 407 T; 0 other;

alignment_scores:
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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182 ArgAlaLeuArgAlaAlaTyrAsnAsnProGluArgAla 194
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604 AGGGCTCTCCGTGCCGTACACACCCCGACGTGCT 642

seq_name: /STDS1/gcgdata/geneseq/geneseqn-emb1/NA001A.DAT:AAK56240

seq_documentation_block:
ID AAK56240 standard; cDNA; 434 BP.
XX
AC AAK56240;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen encoding cDNA SEQ ID NO:1300.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 08-NOV-2000; 2000US-0244874.

PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246509.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-483426/52.
 XX
 PT P-PSDB; AAM83459.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Claim 1; SEQ ID NO 1300; 3071bp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,

CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 434 BP; 120 A; 93 C; 123 G; 93 T; 5 other;
 alignment_scores:
 Quality: 10.00 Length: 10
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-805-550-2 x AAK56240/rev ..
 Align seg 1/1 to reverse of: AAK56240 from: 1 to: 434
 235 LeuProValGlnProSerProAlaSerAla 244
 |||||
 394 CTCCTGCTTCAGCCATCTCCTGCTTCAGCC 365
 seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.AAC20334
 seq_documentation_block:
 ID AAC20334 standard; cDNA: 311 BP.
 XX
 AC AAC20334;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 24409.
 XX
 KW Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 KW
 OS Homo sapiens.
 OS
 PN EP103401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PE 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI: 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 24409; 71bp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX Sequence 311 BP; 103 A; 73 C; 58 G; 76 T; 1 other;
SQ

alignment_scores:

Quality: 9.00 Length: 9
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x AAC20334/rev ..

Align seg 1/1 to reverse of: AAC20334 from: 1 to: 311

334 GlyGlyProGlyGlyAsnIleuGly 342
|||||
116 GGTGGACCTGGGGCAATATTTTGGGG 90

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL17109

seq_documentation_block:

ID ABL17109 standard; DNA; 864 BP.

XX ABL17109;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2800.

KM Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ds.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -

PS Claim 1; SEQ ID NO 2800; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 864 BP; 228 A; 260 C; 213 G; 163 T; 0 other;
SQ

alignment_scores:

Quality: 9.00 Length: 9
Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x ABL17109 ..

Align seg 1/1 to: ABL17109 from: 1 to: 864

132 AlaAlaProAlaValThrValAlaAla 140
|||||
330 GCAGCACCAGCAGCAACAGTTGCTGCA 356

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL25527

seq_documentation_block:

ID ABL25527 standard; DNA; 1464 BP.

XX ABL25527;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28054.

KM Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ds.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -

PS Claim 1; SEQ ID NO 28054; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1464 BP; 332 A; 427 C; 345 G; 360 T; 0 other;
SQ

alignment_scores:

Quality: 9.00 Length: 9
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x ABL25527 ..

Align seg 1/1 to: ABL25527 from: 1 to: 1464

99 PROCAIAlAProValAlAProAlaAla 107
 |||
 472 CCYGTCTCTCTGTCTCTCGCTGCC 498

seq_name: /SIDSL/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH73004

seq_documentation_block:

ID AAH73004 standard; cDNA; 1536 BP.

AAH73004;

19-SEP-2001 (first entry)

Human cervical cancer marker nucleic acid 4278.

Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

Homo sapiens.

WO200142467-A2.

14-JUN-2001.

08-DEC-2000; 2000WO-US33312.

08-DEC-1999; 99US-0169681.

21-DEC-1999; 99US-0171350.

14-MAR-2000; 2000US-0189315.

12-MAY-2000; 2000US-0203791.

09-JUN-2000; 2000US-0210600.

21-JUL-2000; 2000US-0220114.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI; 2001-375006/39.

New isolated nucleic acid for diagnosing and treating cervical cancer

and for assessing and detecting compounds for treating the cancer -

Claim 1; Page 941; 1051pp; English.

The invention relates to novel genes (AAH68727-AAH73863) associated with

cervical cancer with cytostatic activity. The nucleic acids and encoded

polypeptides are useful: to assess if a patient is afflicted with

cervical cancer or has a pre-malignant condition; to monitor the

progression of cervical cancer or a premalignant condition in a patient;

and to select and/or assess the efficacy of a compound or therapy for

inhibiting cervical cancer in a patient. The nucleic acids may also be

useful for gene therapy.

Sequence 1536 BP; 405 A; 506 C; 345 G; 279 T; 1 other;

alignment_scores:

Quality: 9.00 Length: 9

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

US-09-805-550-2 x AAH73004 ..

Align seg 1/1 to: AAH73004 from: 1 to: 1536

81 SerSerGlyAlaSerThrAlaThrThr 89

|||||

1225 TCCAGTGGGCCGACACGCCACCACC 1251

seq_name: /SIDSL/gcdata/geneseq/geneseqn-emb1/NA2001B.DAT:AA564584

seq_documentation_block:

ID AA564584 standard; cDNA; 2307 BP.

AA564584;

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #388.

Human; chromosome mapping; gene mapping; gene therapy; forensic;

food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dzmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

P-PSDB; ABG00397.

New isolated polynucleotide and encoded polypeptides, useful in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits and to assess

biodiversity -

Claim 1; SEQ ID No 388; 103pp; English.

The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes,

polymerase chain reaction (PCR) primers, oligomers, and for chromosome

and gene mapping, and in recombinant production of (II). The

polynucleotides are also used in diagnostics as expressed sequence tags

for identifying expressed genes. (I) is useful in gene therapy techniques

to restore normal activity of (II) or to treat disease states involving

(II). (II) is useful for generating antibodies against it, detecting or

quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

amino acid sequences. AA564197-AA594564 represent novel human

CC Note: The sequence data for this patent did not appear in the printed

specification, but was obtained in electronic format directly from WIPO

at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 2307 BP; 406 A; 587 C; 752 G; 562 T; 0 other;

alignment_scores:

Quality: 9.00 Length: 9

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

US-09-805-550-2 x AA564584/rev ..

Align seg 1/1 to reverse of: AA564584 from: 1 to: 2307

81 SerSerGlyAlaSerThrAlaThrThr 89

|||||

1197 TCCAGTGGGCCGACACGCCACCACC 1171

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAS94336

seq_documentation_block:

ID AAS94336 standard; cDNA; 2633 BP.

AC AAS94336;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #30140.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN MO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG30149.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 1; SEQ ID NO 30140; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC SQ Sequence 2633 BP; 439 A; 713 C; 825 G; 656 T; 0 other;

alignment_scores:

Quality: 9.00 Length: 9
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x AAS94336/rev ..

Align seq 1/1 to reverse of: AAS94336 from: 1 to: 2633

81 SerSerGlyAlaSerThrAlaThrThr 89
|||||
1523 TCCAGTGGGGCCACGACGACGACCC 1497
